

```

1 MPARRLLLLLLPGLGIFGSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||||
1 MPARRLLLLLLPGLGIFGSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||||
51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100
  |||||
51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100
  |||||
101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQTLSAFADSLCPS 150
  |||||
101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQTLSAFADSLCPS 150
  |||||
151 TSLLYLGRTEYTTIMYDTKTRELWNATYFDYAASLPEDEGDYKMSHFVS 200
  |||||
151 TSLLYLGRTEYTTIMYDTKTRELWNATYFDYAASLPEDEGDYKMSHFVS 200
  |||||
201 NGDGLVVTVDSEGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVEL 250
  |||||
201 NGDGLVVTVDSEGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVEL 250
  |||||

```

FIG. 1

103230 1511200

```

251 RYLTMSGEVGRITWKYPPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300
|||||
251 RYLTMSGEVGRITWKYPPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300
|||||
301 HEGVAVVPRGSTLP LLEGPTDGV TIGDKGECVITPSTDVKFDPGLKSKN 350
|||||
301 HEGVAVVPRGSTLP LLEGPTDGV TIGDKGECVITPSTDVKFDPGLKSKN 350
|||||
351 KLNILRNWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400
|||||
351 KLNILRNWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400
|||||
401 EE..TLLQMTS 409
|| :|::||
401 EEVINLVDQTS 411

```

FIG. 1 (CONT.¹)

5 QLQSVSSAIHLCDDKKMELSLNIPVNHGPOEESCGSSQLHENS GSPETSR 54
:|||||
313 KLQSVSSAIHLCDDKKMELSLNIPVNHGPOEESCGSSQLHENS GSPETSR 362
55 SLPAPQDNDFLSRKAQDCYFMKLHHCPCGNHSHWDSTISGSQRAAFCDHKT 104
|||||
363 SLPAPQDNDFLSRKAQDCYFMKLHHCPCGNHSHWDSTISGSQRAAFCDHKT 412
105 PCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQMT EACLNQSLDA 154
|||||
413 PCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQMT EACLNQSLDA 462
155 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDTIQGE EFAKVIVQKLKDN 204
|||||
463 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDTIQGE EFAKVIVQKLKDN 512
205 KQMGLOQPYPEILVVSRSPSLNLLQNKSM 232
|||||
513 KQMGLOQPYPEILVVSRSPSLNLLQNKSM 540

FIG. 2

105200 1984260

```

1  MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSVMQKYLEDR 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSVMQKYLEDR 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 RVARSR EIFDSYIMKELLACSHPF SKSATEHVQHLGKKQVPPDLFQPYI 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 RVARSR EIFDSYIMKELLACSHPF SKSATEHVQHLGKKQVPPDLFQPYI 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 EEICQNLRGDVFQKFIE 167
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 EEICQNLRGDVFQKFIE 167

```

FIG. 3

```

1  MGLVSSKKPDKEKPIKEDKGQWSPLKVSQDKDAPPLPPLVVFVFNHLTPP 50
   |||||
1  MGLVSSKKPDKEKPIKEDKGQWSPLKVSQDKDAPPLPPLVVFVFNHLTPP 50
   |||||
51 PPDEHLEDKHFVVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARS 100
   |||||
51 PPDEHLEDKHFVVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARS 100
   |||||
101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
   |||||
101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
   |||||
151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYIISPRITFPSLQA 200
   |||||
151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYIISPRITFPSLQA 200
   |||||
201 LVQHYS..... 206
   |||||
201 LVQHYSKKGDLGCQRLTLPVCRPAPQNPWAQDEWELPRQSLRIVRKLGS 250
   |||||
207 .....SYKNNMKVAIKTLKEGTSPEAFGEANVMKAIQHERLVR 249
   : |||||
251 QFGEVMMGYKNNMKVAIKTLKEGTSPEAFGEANVMKAIQHERLVR 300

```

FIG. 4

250 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRISLPRLLIDMSAQIAEGMAY 299
 |||||
 301 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRISLPRLLIDMSAQIAEGMAY 350
 |||||
 300 IERMNSIHRDLRAANILVSEALCCKIADFGRLARIIDSEYTAQEGAKFPIK 349
 |||||
 351 IERMNSIHRDLRAANILVSEALCCKIADFGRLARIIDSEYTAQEGAKFPIK 400
 |||||
 350 WTAPEAIHFGVFTIKADVWSFGVLLMEVVTYGRVPYPGMSNPEVIRNLER 399
 |||||
 401 WTAPEAYHFGVFTIKADVWSFGVLLMEVVTYGRVPYPGMSNPEVIRNLER 450
 |||||
 400 GYRMPRPDTCPPELYRGVIAECWRSRPEERPTFEFLQSVLEDFYTATERQ 449
 |||||
 451 GYRMPRPDTCPPELYRGVIAECWRSRPEERPTFEFLQSVLEDFYTATERQ 500

450 YELQP 454

||||

501 YELQP 505

FIG. 4 (CONT.)

```

1  MENFQVEKIGEGTYGVVYKARKNLGGEVVALKKIRLDTETEGVPSTAIR 50
  |||||
1  MENFQVEKIGEGTYGVVYKARKNLGGEVVALKKIRLDTETEGVPSTAIR 50
  |||||

51  EISLLKELNHPNIVKLLDVIHTENK 75
  |||||
51  EISLLKELNHPNIVKLLDVIHTENK 75
  |||||

```

FIG. 5

```

1 MTRDEALPDHSAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
  |||||
1 MTRDEALPDHSAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
  |||||
51 IDVTGGGSFSPPEVRELREALTLKEVDILRKVSGHPNISIQLKDTYETNTF 100
  |||||
51 IDVTGGGSFSPPEVRELREALTLKEVDILRKVSGHPNI.IQLKDTYETNTF 99
  |||||
101 FFLVFDLMKRGELFD 115
  |||||
100 FFLVFDLMKRGELFD 114

```

FIG. 6

FIG. 7

22 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENWPFGSKLPLVG 71
 |||||
 197 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENWPFGSKLPLVG 246
 |||||
 72 QYSLRKQPYNNLKHKFPWLSEAGIRLLHFLFMYDPKKRATAGDCLESSYF 121
 |||||
 247 QYSLRKQPYNNLKHKFPWLSEAGIRLLHFLFMYDPKKRATAGDCLESSYF 296
 |||||
 122 KEKPLRLPISGVCEGCREPG 141
 |||||
 297 KEKPLRLPISGVCEGCREPG 316

FIG. 8

```

1 VFLGRCSVKFEFEKINRIGEGTYGIYRARDTQTDEIVALKKVRMDKEK 50
  |||||
1 VFLGRCSVKFEFEKINRIGEGTYGIYRARDTQTDEIVALKKVRMDKEK 50
  |||||

51 GIPISLREITLLRLRHPNII 72
  |||||
51 GIPISLREITLLRLRHPNIV 72
  |||||

```

FIG. 9

```

1 MGEAEKFHYISCDLDINVLKIGSLEGRQKS YKAVLEDPMLKFSGLY 50
| | | | | | | | | | | | | | | | : | | | | | | | | | |
1 MGEAEKFHYISCDLDINVLKIGSLEGRQKS YNAVLEDPMLKFSGLY 50
| | | | | | | | | | | | | | | | : | | | | | | | | | |
51 QETCSDLVYCQFAEGKPALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 QETCSDLVYCQFAEGKPALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 PRNAQVALTIWDVYGPKAVPVGGTTVSFLGKYGMFRQGMHDLKVWP NVE 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 PRNAQVALTIWDVYGPKAVPVGGTTVSFLGKYGMFRQGMHDLKVWP NVE 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 ADGSEPTKTPGRTSSLTSEDQMSRLAKLTKAHRQGHMV KVDWLDR LTFRE 200
| | | | | : | | | | | | | | | | | | | | | | | | | | | |
151 ADGSEPTKTPGRTSSLTSEDQMSRLAKLTKAHRQGHMV KVDWLDR LTFRE 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 IEMINESVKRSSNFMYLMGGFCVKDDKEYGI VYEKGDESPIL TSF 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 IEMINESVKRSSNFMYLMGGFCVKDDKEYGI VYEKGDESPIL TSF 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 ELVKVPDQPOMSL ENLVESKHNNLP RSLRSGPSDH DLKPYPSP RDQLKNIV 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 ELVKVPDQPOMSL ENLVESKHNNLP RSLRSGPSDH DLKPYPSP RDQLKNIV 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

FIG. 10

301	SYPPSKPPTYEEQDLVWFEFRYYLTNQDKALTKILTTSVIWDLPOEAKQALA	350
301	SYPPSKPPTYEEQDLVWFEFRYYLTNQDKALTKILTTSVIWDLPOGAKQALA	350
351	LLGKNWPMDDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLLQLV	400
351	LLGKNWPMDDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLSQLV	400
401	QALKYENFDDIKNGLEPTKKDSQSSVSNVSGNSGINSAEIDSSQIITSPL	450
401	QALKYENFDDIKNGLEPTKKDSQSSVSGNVSGNSGINSAEIDSSQIITSPL	450
451	PSVSSPPPPASKTKEVPDGENLEQDICTFLISPACKNSTLANLYLYWYVIVE	500
451	PSVSSPPPPASKTKEVPDGENLEQDICTFLISPACKNSTLANLYLYWYVIVE	500
501	CEDQDQTQORDPKTHEMYLNVMMRRFSQALLKGDKSVRMRSLLAAQQT FVD	550
501	CEDQDQTQORDPKTHEMYLNVMMRRFSQALLKGDKSVRMRSLLAAQQT FVD	550

FIG. 10 (CONT.)¹

```

551 RLVHLMKAVQRESGNRKKNERLQALLGDNEKMNLSDVELLPLEPQVK 600
|||||
551 RLVHLMKAVQRESGNRKKNERLQALLGDNEKMNLSDVELLPLEPQVK 600
|||||
601 IRGII PETATL FKSALMPAQLFFKTEDGCKYPVIFKHGDDDLRQDQILQI 650
|||||
601 IRGII PETATL FKSALMPAQLFFKTEDGCKYPVIFKHGDDDLRQDQILQI 650
|||||
651 ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTESI 700
|||||
651 ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTESI 700
|||||
701 QNFFRKYAPSENGPNCISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLL 750
|||||
701 QNFFRKYAPSENGPNCISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLL 750
|||||
751 LTKTG 755
|||||
751 LTKTG 755

```

FIG. 10 (CONT. ²)

FIG. 11

301 SYPPSKPPTYEEQDLVWEFRYILTQDKALTKILTSTVIWDLPOEAKQALA 350
 |||||
 301 SYPPSKPPTYEEQDLVWEFRYILTQDKALTKILTSTVIWDLPOGAKQALA 350
 |||||
 351 LLGKNPMDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLLQLV 400
 |||||
 351 LLGKNPMDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLSQLV 400
 |||||
 401 QALKYENFDDIKNGLEPTKKDSQSSVSENVNSGINSAEIDSSQIITSPL 450
 |||||
 401 QALKYENFDDIKNGLEPTKKDSQSSVSENVNSGINSAEIDSSQIITSPL 450
 |||||
 451 PSVSSPPPPASKTKEVPDGENLEQDLCTFLISPRACKNSTLANYLYWYVKII 500
 |||||
 451 PSVSSPPPPASKTKEVPDGENLEQDLCTFLISPRACKNSTLANYLYWYV.IV 499
 |||||

FIG. 11 (CONT.)¹


```

1  MGNAAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50
  |||||
1  MGNAAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50
  |||||
51 GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100
  |||||
51 GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100
  |||||
101 FPFLVKLEFSFKDNSNLYMMEYVPPGGEMFSLRLRIGRF 139
  |||||
101 FPFLVKLEFSFKDNSNLYMMEYVPPGGEMFSLRLRIGRF 139
  |||||

```

FIG. 12

```

1  MVFENGLKIKICEAVSLKPTAWSLRHAVGPRPQTFLLDPYIALNVDDSR 50
  |||||
1  MVFENGLKIKICEAVSLKPTAWSLRHAVGPRPQTFLLDPYIALNVDDSR 50
  |||||
51 IGQTATKQKTNSPAWHDEFVTDVCNGRKTIELAVFHDAPIGYDDFVANCTI 100
  |||||
51 IGQTATKQKTNSPAWHDEFVTDVCNGRKTIELAVFHDAPIGYDDFVANCTI 100
  |||||
101 QFEELLQNGSRHFEDWIDLEPEGRVYVVIIDLSGSSGEVKIPNSAFCEER 150
  |||||
101 QFEELLQNGSRHFEDWIDLEPEGRVYVVIIDLSGSSGEAPKDNEERVFRER 150
  |||||
151 VEMR 154
  :: |
151 MRPR 154

```

FIG. 13

1	MILIPRMLLVFLLLPILSSAKAQNPAICRYPLGMSGGQIPDEDITASS	50
1	MILIPRMLLVFLLLPILSSAKAQNPAICRYPLGMSGGQIPDEDITASS	50
51	QWSESTAACYGRLDSEEGDGAWCPEIPVEPDDLKEFLQIDLHLHLFITLV	100
51	QWSESTAACYGRLDSEEGDGAWCPEIPVEPDDLKEFLQIDLHLHLFITLV	100
101	GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI	150
101	GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI	150
151	FLKLEPPIVARFVRFIPVTDHSMNVCMRVELYGCVWL DGLVSYNAPAGQ	200
151	FLKLEPPIVARFVRFIPVTDHSMNVCMRVELYGCVWL DGLVSYNAPAGQ	200
201	QFVLPGGSIIYLNDSVYDGA VYSMT EGLQLTDGVSGLDDFTQTHEYHV	250
201	QFVLPGGSIIYLNDSVYDGA VYSMT EGLQLTDGVSGLDDFTQTHEYHV	250
251	WPGYDVYGVWRNESATNGYIEIMFEFDRI RNF TTMKVHCNNMFAKV KIFK	300
251	WPGYDVYGVWRNESATNGYIEIMFEFDRI RNF TTMKVHCNNMFAKV KIFK	300

FIG. 14

```

301 EVQCYRSEASEWEPNAISFPLVLDVNP SARFVTVPLHHRMASAIKCQY 350
    |||||||
301 EVQCYRSEASEWEPNAISFPLVLDVNP SARFVTVPLHHRMASAIKCQY 350
    |||||||
351 HFADTWMFSEITFQSDAAMYNNSALPTSPMAPTYDPM LKVDDSNTRI 400
    |||||||
351 HFADTWMFSEITFQSDAAMYNNSALPTSPMAPTYDPM LKVDDSNTRI 400
    |||||||
401 LIGCLVAIIFILLAIIVILWRQFWQKMLEKASRRMLDDEMTVSLSPSD 450
    |||||||
401 LIGCLVAIIFILLAIIVILWRQFWQKMLEKASRRMLDDEMTVSLSPSD 450
    |||||||
451 SSMFNRRSSSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE 500
    |||||||
451 SSMFNRRSSSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE 500
    |||||||
501 SG.....EDDVVE.QGVKGETSASI 519
    ||      | :|: | | | :|: | :|:
501 SGCSGVVKVPQPSGPEGVPHYAEADIVNLQGV TGGNTYSV 540

```

FIG. 14 (CONT.)¹

```

1 MANFQEHLSGSSPHLPFSEKTFNGLQDELTA MGNHPSPKLLEDQOEKG 50
|||||
1 MANFQEHLSGSSPHLPFSEKTFNGLQDELTA MGNHPSPKLLEDQOEKG 50
|||||
51 MVRTELIESVHSPVTTVLT SVSEDSRDQFENSVLQREHDESETAVSQG 100
|||||
51 MVRTELIESVHSPVTTVLT SVSEDSRDQFENSVLQREHDESETAVSQG 100
|||||
101 NSNTVDGESTGTE DIKIQFSRSGSGGFLEGLFGCLRPVWNII GKAYS 150
|||||
101 NSNTVDGESTGTE DIKIQFSRSGSGGFLEGLFGCLRPVWNII GKAYS 150
|||||
151 TDYKFMQQDTWEVPFEEISELQWLGSAQGA VFLGKFRAE EVAIKKVREQ 200
||||:|||||
151 TDYKLQQQDTWEVPFEEISELQWLGSAQGA VFLGKFRAE EVAIKKVREQ 200
|||||
201 NETDIKHLRLKHPNII AFKGVCTQAPCYCI IMEYCAHGQLYEVLRA GRK 250
|||||
201 NETDIKHLRLKHPNII AFKGVCTQAPCYCI IMEYCAHGQLYEVLRA GRK 250
|||||
251 ITPRLLVDSWTGIASGMNYLHLHKIIHRDLKSP 283
|||||
251 ITPRLLVDSWTGIASGMNYLHLHKIIHRDLKSP 283

```

FIG. 15

```

21 KSGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 70
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
295 EGNKKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 344
   . . . . .
71 GGSVIKYSKNTRKQWLKETPDTLNLILKNADLSIAFQTYTYIRPGSEGF 120
   |::::::::::::::::::::::::::::::::::::::::::::::::::::
345 GGSVIKYSKNTRKQWLKETPDTLNLILKNADLSIAFQTYTYIRPGSEGF 394
   . . . . .
121 LKGPLSEETEASDSVDGGHDSVILDPERLEPGLDEEDTDFEEDDNPDPWV 170
   |::::::::::::::::::::::::::::::::::::::::::::::::::::
395 LKGPLSEETEASDSVDGGHDSVILDPERLEPGLDEEDTDFEEDDNPDPWV 444
   .
171 SELKKRAGWQGLCDR 185
   |::::::::::::::::
445 SELKKRAGWQGLCDR 459

```

FIG. 16

1 MAPPSEETPLIPQRCSLLSTEAGALHVLLPARGPGPPQRLSFSFG 46
|||||
1 MAPPSEETPLIPQRCSLLSTEAGALHVLLPARGPGPPQRLSFSFG 46

FIG. 17

```

1 MAESACASSFFPLVLLLAGSGSGPRGVQALLCACTSCLOANYTCETDG 50
  |||||
1 MAESACASSFFPLVLLLAGSGSGPRGVQALLCACTSCLOANYTCETDG 50
  |||||
51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSS EDLRNTHCCYTDY 100
  |||||
51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSS EDLRNTHCCYTDY 100
  |||||
101 CNRIDLRVPSGHLKEPEHPSMMWGPVELVGIIAGPVFLFLIIIVFLVIN 150
  |||||
101 CNRIDLRVPSGHLKEPEHPSMMWGPVELVGIIAGPVFLFLIIIVFLVIN 150
  |||||
151 YHQRVYHNQRQLMEDPSC EMCLSKDKTLQDLVYDLSTSGSGSGTKFF 198
  |||||
151 YHQRVYHNQRQLMEDPSC EMCLSKDKTLQDLVYDLSTSGSGSGGLPLF 198
  |||||

```

FIG. 18


```

1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
|||||
1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
|||||
51 HNGERRIIAFSRPVKYEDVEHKVTVTFGQPLDLHYMNNELSILLKNQDDL 100
|||||
51 HNGERRIIAFSRPVKYEDVEHKVTVTFGQPLDLHYMNNELSILLKNQDDL 100
|||||
101 DKAIIDLRSSSMKSLRILLLSQDRHNHSSSPHSEVSRQVRIKASQSAGD 150
|||||
101 DKAIIDLRSSSMKSLRILLLSQDRHNHSSSPHSEVSRQVRIKASQSAGD 150
|||||
151 INTIYQPPEPRSRHLVSSSQNPGRSSPPPGYVPERQQHARQGSYTSINS 200
|||||
151 INTIYQPPEPRSRHLVSSSQNPGRSSPPPGYVPERQQHARQGSYTSINS 200
|||||
201 EGEFIPETSEQCMLDPLSSAENSLSGCQSLDRSADSPSFRKSRMSRAQS 250
|||||
201 EGEFIPETSEQCMLDPLSSAENSLSGCQSLDRSADSPSFRKSRMSRAQS 250
|||||

```

FIG. 19

```

251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRTTFPRIR 300
    |||||
251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRTTFPRIR 300
    |||||
301 HQGNLFTLVPSRSLSTNGENMGLAVQYLDPRGRRLRSADSENALSVQERN 350
    |||||
301 HQGNLFTLVPSRSLSTNGENMGLAVQYLDPRGRRLRSADSENALSVQERN 350
    |||||
351 VPTKCEELSLARRRLPRWSQTSYGGKQLG 379
    ||| : ||
351 VPTKSPSAPINWRR.....GKLLG 369

```

FIG. 19 (CONT.¹)

```

1 MDEQFALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQKKHNSSSS 50
  |||||||
1 MDEQFALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQ..... 42

51 ALLNSPTVTSSCAGASEKKKFLSDVRIKFEHNGERRIIAFSRPVKYEDV 100
  |||||||
43 .....SDVRIKFEHNGERRIIAFSRPVKYEDV 69

101 EHKVTTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSSMKSIRIL 150
  |||||||
70 EHKVTTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSSMKSIRIL 119

151 LLSQDRNHNSSPHSEVSRQVRIKASQAGDINTIYQPEPRSRHLSVSS 200
  |||||||
120 LLSQDRNHNSSPHSEVSRQVRIKASQAGDINTIYQPEPRSRHLSVSS 169

201 QNPGRSSPPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 250
  |||||||
170 QNPGRSSPPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 219

```

FIG. 20

```

251 AENSLGSCQSLDRSADSPSFRKSRMSRAQSFEDNQRQEYSDRETQLYDKG 300
    |||||
220 AENSLGSCQSLDRSADSPSFRKSRMSRAQSFEDNQRQEYSDRETQLYDKG 269
    |||||
301 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSRSLSLSTNG 350
    |||||
270 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSRSLSLSTNG 319
    |||||
351 ENMGLAVQYLDPRGRLRSADSENALSVQERNVPTKCEELSLARRRLPRWS 400
    |||||
320 ENMGLAVQYLDPRGRLRSADSENALSVQERNVPTKSPSAPINWRR..... 364
    ||||
    401 QTSYGGKQLG 410
    365 .....GKLLG 369

```

FIG. 20 (CONT.¹)

```

1 MAKQDSVECPFCDEVSKYEKLAKIGQTFGEVFKARHRTGQKVALKKV 50
  |||||
1 MAKQDSVECPFCDEVSKYEKLAKIGQTFGEVFKARHRTGQKVALKKV 50
  |||||
51 LMENEKEGFPITALREIKIQLLKHENVVNLIIEICRTKASPNRCKGSIY 100
  |||||
51 LMENEKEGFPITALREIKIQLLKHENVVNLIIEICRTKASPNRCKGSIY 100
  |||||
101 LVDFCEHDLAAGLLSNVLVKFTLSEIKRVMQMLNGLIYY..... 139
  |||||
101 LVDFCEHDLAAGLLSNVLVKFTLSEIKRVMQMLNGLIYYIHRNKILHRDM 150
  |||||
139 ..... 139
151 KAANVLITRDGVIKLADFLARAFSLAKNSQPNRYTNRVVTLWYRPPPELL 200
  |||||
139 ..... 139
201 LGERDYGPIDLWGAGCIMAEMWTRSPIMQNGTEQHQALALISQLCGSITP 250
  |||||

```

FIG. 21

139 139
 251 EVWPNVDNYELYEKLELVKGQKRKVKDRPKAYVRDPYALDLIDKLVLDP 300
 140NHDFWSDPMPSDLKGMSTHLTSMFEYLAPPRKGSQIT 179
 |||||.....
 301 AQRIDDDALNHDFWSDPMPSDLKGMSTHLTSMFEYLAPPRKGSQIT 350
 180 QOSTNQSRNPATTNQTEFERVF 201
 |||||.....
 351 QOSTNQSRNPATTNQTEFERVF 372

FIG. 21 (CONT.¹)

```

1 MATSRYEPVAEIGVAYGTVYKARDPHSGHFCALKSVRVPNGGGGGGGLP 50
  |||||
1 MATSRYEPVAEIGVAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGGLP 50
  |||||
51 ISTVREVALRRLEAFEHPNVVRLMDVCATSRDREIKVTLVFEHVDQDL 100
  |||||
51 ISTVREVALRRLEAFEHPNVVRLMDVCATSRDREIKVTLVFEHVDQDL 100
  |||||
101 RTYLDKAPPPGLPAETIK 118
  |||||
101 RTYLDKAPPPGLPAETIK 118
  |||||

```

FIG. 22

1 MATSRYPVAEIGVGAYGTVVKARDPHSGHFCALKSVRP 40
 |||||
 1 MATSRYPVAEIGVGAYGTVVKARDPHSGHFVALKSVRP 40

FIG. 23


```

34 PLPLEPRAVYCKDVL DIEQFSTVKG VNL DHTDDDFYSKFSTGVSIPWQN 83
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
464 PFVPDPRAVYCKDVL DIEQFSTVKG VNL DHTDDDFYSKFSTGVSIPWQN 513
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 EMITECFKELNVFGPNGLPPDLNRNHPPPEPKKGLLQRLFKRQHQNNS 133
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
514 EMITECFKELNVFGPNGLPPDLNRNHPPPEPKKGLLQRLFKRQHQNNS 563
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
134 KSSPSSKTSFNHHHINSNVSSNSTGSS 160
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
564 KSSPSSKTSFNHHHINSNVSSNSTGSS 590
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

FIG. 24

```

28  LLSPSGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 77
   ::  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 LDDYGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 367
      .
78  YWGLGCLIIYEMIEGQSPFRGRKEKVKREEVDRLVLETEEVYSHKFSEEA 127
      .
368 YWGLGCLIIYEMIEGQSPFRGRKEKVKREEVDRLVLETEEVYSHKFSEEA 417
      .
128 SICKMLLTDKAQORLGCQEEGAEEVKRHPFFRNMFKRLEAGMLDPFPVP 177
      .
418 SICKMLLTDKAQORLGCQEEGAEEVKRHPFFRNMFKRLEAGMLDPFPVP 467
      .
178 DPRAYCKDVLVDIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPQNEMIE 227
      .
468 DPRAYCKDVLVDIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPQNEMIE 517
      .
228 TECFKELNVFGPNGTLPPDLNRNHPPPEPKKGLQLRLFKRHQNNSKSSP 277
      .
518 TECFKELNVFGPNGTLPPDLNRNHPPPEPKKGLQLRLFKRHQNNSKSSP 567
      .
          278 SSKTSFNHHHINSNVSSNSTGSS 300
              ||||| ||||| ||||| |||||
          568 SSKTSFNHHHINSNVSSNSTGSS 590
```

FIG. 25

1 MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
 |||||
 1 MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
 |||||
 51 MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPSEVTGVSVLAERCKKNNG 100
 |||||
 51 MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPSEVTGVSVLAERCKKNNG 100
 |||||
 101 KAEFWLDLQPOAKVIMSVQYFLEDVCKQSMRSEDEAKFPTMRRGAIKQ 150
 |||||
 101 KAEFWLDLQPOAKVIMSVQYFLEDVCKQSMRSEDEAKFPTMRRGAIKQ 150
 |||||
 151 AKIHYIKNHEFIATFFGQPTFCQSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200
 |||||
 151 AKIHYIKNHEFIATFFGQPTFCQSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200
 |||||
 201 IDKIIGRCTGTAANSRDTIFQKERFNDMPHRFKVHNYMSPTFCDHCGSL 250
 |||||
 201 IDKIIGRCTGTAANSRDTIFQKERFNDMPHRFKVHNYMSPTFCDHCGSL 250
 |||||
 251 LLPAPHDKHQW.....DCG 264
 |
 251 L.....WGLVKQLKCEDCG 265
 |||

FIG. 27

```

1 MDETHPGYKEVDLEFLVSPSLPCLLSFAGSARHLVPPDSNLFSKLWACG 50
  |||||
203 MDETHPGYKEVD.....LWACG 220

51 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 100
  |||||
221 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 270

101 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 150
  |||||
271 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 320

151 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWKKGEOQNR 200
  |||||
321 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWKKGEOQNR 370

201 AALFQHRPPGPFIMGPEEGDSAAITEDEAVILVG 236
  |||||
371 AALFQHRPPGPFIMGPEEGDSAAITEDEAVILVG 406

```

FIG. 28

1	MAFCAKMRSSKKTENVLEAPGPGEVIFYLSDREPLRLGSGEYTAELCI	50
1	MAFCAKMRSSKKTENVLEAPGPGEVIFYLSDREPLRLGSGEYTAELCI	50
51	RAAQACRISPLCHNLFALYDENTKLYAPNRTTIVDDKMSLRLHYMRFY	100
51	RAAQACRISPLCHNLFALYDENTKLYAPNRTTIVDDKMSLRLHYMRFY	100
101	FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG	150
101	FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG	150
151	QYDLVKCLAPIRDPKTEQDGHDIENECIGMAVLAI SHYAMMKMQLPELP	200
151	QYDLVKCLAPIRDPKTEQDGHDIENECIGMAVLAI SHYAMMKMQLPELP	200
201	KDISYKRYIPETLNKSIRQRNLLTRMRINNVEKDFLKEFNKNTICDSSVS	250
201	KDISYKRYIPETLNKSIRQRNLLTRMRINNVEKDFLKEFNKNTICDSSVS	250
251	THDLKVKYLATLETITKHYGAEIFETSMLLISSENEMNWFHSDNGGNVLY	300
251	THDLKVKYLATLETITKHYGAEIFETSMLLISSENEMNWFHSDNGGNVLY	300

FIG. 29

[illegible]

FIG. 29 (CONT.)¹⁾

FIG. 30

1 MGCVCCKEATKLTEERDGSNQSSGYRGTDTPQHYPFSGVTSIPNY 50
 |||||
 1 MGCVCCKEATKLTEERDGSNQSSGYRGTDTPQHYPFSGVTSIPNY 50
 |||||
 51 NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGVTLFVALYDYEARTEDD 100
 |||||
 51 NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGVTLFVALYDYEARTEDD 100
 |||||
 101 LSFHKGEKFFQILNSSEGDWEARSLTTGETGYTPSNYVAPVDSIQAEWY 150
 |||||
 101 LSFHKGEKFFQILNSSEGDWEARSLTTGETGYTPSNYVAPVDSIQAEWY 150
 |||||
 151 FGKLGKDAERQLLSFGNPRGTFLIRESSTTKGAYSLSIRDWDDMKGDHV 200
 |||||
 151 FGKLGKDAERQLLSFGNPRGTFLIRESSTTKGAYSLSIRDWDDMKGDHV 200
 |||||
 201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
 |||||
 201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
 |||||

FIG. 31

```

251 PRLDLSVKT KDVEI PRES LQLIKRLGNGQFGEVMMGTWNGNTKVAIKT 300
    |||||
251 PRLDLSVKT KDVEI PRES LQLIKRLGNGQFGEVMMGTWNGNTKVAIKT 300
    |||||

301 LKPGTMSPE SFLEEAQIMKKLKHDKLVQLYAVVSEEPYIVTEYMNKG 348
    |||||
301 LKPGTMSPE SFLEEAQIMKKLKHDKLVQLYAVVSEEPYIVTEYMNKG 348
    |||||

```

FIG. 31 (CONT.¹)

50 SLELHKRRKALTEPEARYYLRQIVLGCQYLHNRNVIHRDLKLGNLFLNE 99
 |||
 137 SLELHKRRKALTEPEARYYLRQIVLGCQYLHNRNVIHRDLKLGNLFLNE 186
 |||
 100 DLEVKIGDFGLATKVEYDGERKKTLCGTPNYIAPEVLSKKGHSFEVDVWS 149
 |||
 187 DLEVKIGDFGLATKVEYDGERKKTLCGTPNYIAPEVLSKKGHSFEVDVWS 236
 |||
 150 IGCIMYTLLVGKPPFETSCCLKETYLRIKKNEYSIPKHINPVAASLIQKML 199
 |||
 237 IGCIMYTLLVGKPPFETSCCLKETYLRIKKNEYSIPKHINPVAASLIQKML 286
 |||
 200 QTDTARPTINELLNDEFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 249
 |||
 287 QTDTARPTINELLGDEFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 336
 |||
 250 RKPLTVLNKGLENPLPERPREKEEPVVRETGEVVDCHLSDMLQQLHSVNA 299
 |||
 337 RKPLTVLNKGLENPLPERPREKEEPVVRETGEVVDCHLSDMLQQLHSVNA 386
 |||

FIG. 32

```

300 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSKYGLGYQLCDNSVGVL 349
|||||
387 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSKYGLGYQLCDNSVGVL 436
|||||
350 NDSTRLLYNDGDSLQYIERDGTESYLTVSSHPNSLMKKITLLKYFRNYM 399
|||||
437 NDSTRLLYNDGDSLQYIERDGTESYLTVSSHPNSLMKKITLLKYFRNYM 486
|||||
400 SEHLKAGANITPREGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 449
|||||:|||||
487 SEHLKAGGNITPRQGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 536
|||||
450 DHTKLIPLMAAVTYIDEKRDFTYRLSLLEEYGCCKELASRLRYARTM 499
|||||
537 DHTKLIPLMAAVTYIDEKRDFTYRLSLLEEYGCCKELASRLRYARTM 586
|||||
500 VDKLLSSRSASNRLKAS 516
|||||
587 VDKLLSSRSASNRLKAS 603

```

FIG. 32 (CONT.¹)

FIG. 33

FIG. 34

FIG. 35

167 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 216
 |||||
 1 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 50

217 PEEKKTATQLHSKRRPK 233
 |||||:
 51 PEEKKTATQLHSKRRPK 67

FIG. 36


```

1  MSAKVRILKKLEQLLLDGPWRNESALSVEITLIDLVLCLYTECSHSALRRDK 50
  |||
1  MSAKVRILKKLEQLLLDGPWRNESALSVEITLIDLVLCLYTECSHSALRRDK 50
  |||
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIVIGRGAFGEVAVVKMKNTER 100
  |||
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIVIGRGAFGEVAVVKMKNTER 100
  |||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAIIDSIHQLHYVHRD 200
  |||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAIIDSIHQLHYVHRD 200
  |||
201 IKPDNVLLDVNGHIRLADEGSLKMNDDGTQSSVAVGTPDYISPEILQA 250
  |||
201 IKPDNVLLDVNGHIRLADEGSLKMNDDGTQSSVAVGTPDYISPEILQA 250
  |||

```

FIG. 37

```

251 MEDGMGKYGPECDWWSLGVCMYEMLYGETPFYAESLIVETYGKIMNHEERF 300
    |||||||||||||||||||||||||||||||||||||||||||||||
251 MEDGMGKYGPECDWWSLGVCMYEMLYGETPFYAESLIVETYGKIMNHEERF 300

    301 QFPSHVTDVSEEAKDLIQRLSC 322
        |||||||||||||||||||
    301 QFPSHVTDVSEEAKDLIQRLIC 322

```

FIG. 37 (CONT.¹)

403210 434463

```

1  MSKVRLLKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECHSALRRDK 50
   |||||
1  MSKVRLLKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECHSALRRDK 50
   |||||
51 YVAEFLEWAKPTQLVKEMQLHREDFEI IKVIGRGAFGEVAVVMKNTER 100
   |||||
51 YVAEFLEWAKPTQLVKEMQLHREDFEI IKVIGRGAFGEVAVVMKNTER 100
   |||||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
   |||||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
   |||||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRD 200
   |||||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRD 200
   |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231
   |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231

```

FIG. 38

```

1 MELRVGNRYRLGRKIGSGSFGDIYL..... 25
  |||||
1 MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLH 50
26 .....VGIPTRWCGAEGDYNVMVMELLGPSLEDLNFNFCSRKF 63
  |||||
51 IESKIYKMQGGVGIPTRWCGAEGDYNVMVMELLGPSLEDLNFNFCSRKF 100
64 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFMGLGKKGNLVYIIDF 113
  |||||
101 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFMGLGKKGNLVYIIDF 150
114 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLESIG 163
  |||||
151 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLESIG 200
164 YVIMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSFAT 213
  |||||
201 YVIMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSFAT 250

```

FIG. 39

708 4000

FIG. 39 (CONT.¹)

```

14 TFAAPSFDDKILEVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 63
   |||||
817 TFAAPSFDDKILEVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 866
   |||||
64 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEDKQKCEL 113
   |||||
867 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEDKQKCEV 916
   |||||
114 PRPSCSLHPPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMQEOLA 163
   |||||
917 PRPSCSLHPPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMQEOLA 966
   |||||
164 HAVNASSKSMDRVYGKPRTEGLNCFSVLEMVNNFRALRSETELLSSGKM 213
   |||||
967 HAVNASSKSMDRVYGKPRTEGLNCFSVLEMVNNFRALRSETE.LLSGKM 1015
   |||||
214 ALQLDPPQKEQLGSALAEMDRQLRRLADTPWLCQSAEPGDEESVMLDLAK 263
   |||||
1016 ALQLDPPQKEQLGSALAEMDRQLRRLADTPWLCQSAEPGDEESVMLDLAK 1065

```

FIG. 40

264 RSRSGKFRFLVTKFKEKNNKKEAHSSLGAPVHLWGTEEVAAWLEHLSL 313
 |||||
 1066 RSRSGKFRFLVTKFKEKNNKKEAHSSLGAPVHLWGTEEVAAWLEHLSL 1115
 |||||
 314 EYKDIFTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA 363
 |||||
 1116 EYKDIFTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA 1165
 |||||
 364 AVEA 367
 |||||
 1166 AVEA 1169

FIG. 40 (CONT.¹)

FIG. 41

1	MIVHDDVESEPA	MTSKEGTLIVRQ	TQSASSTLQKHKSSSF	TFIDPRL	50
751	MIVHDDVESEPA	MTSKEGTLIVRQ	TQSASSTLQKHKSSSF	TFEIDPRL	800
51	LQISPSSGTTVTS	VVGFCDMRPEAIRQD	PTRKGSVVVNPNTP	NTRPQSD	100
801	LQISPSSGTTVTS	VVGFCDMRPEAIRQD	PTRKGSVVVNPNTP	NTRPQSD	850
101	TPEIRKYKKRFNSEILCAALGWGNLLVGTESGLMLLDRSGQGKVYPLINR				150
851	TPEIRKYKKRFNSEILCAALGWGNLLVGTESGLMLLDRSGQGKVYPLINR				900
151	RRFQQMDVLEGLNVLTISGKKDKLRVYLSWLNRKILHNDPEVEKKQGW				200
901	RRFQQMDVLEGLNVLTISGKKDKLRVYLSWLNRKILHNDPEVEKKQGW				950
201	TTVGDLEGCVHYKVKYERIKFLVIALKSSVEVYAWAPKPYHKFMATKSF				250
951	TTVGDLEGCVHYKVKYERIKFLVIALKSSVEVYAWAPKPYHKFMATKSF				1000

FIG. 42

FIG. 42 (CONT.¹)

14 GEVDLTALAKELRAVEDVRPHKVTDYSSSESGTTDEEDDDVEQEGAD 63
 |||||
 674 GEVDLTALAKELRAVEDVRPHKVTDYSSSESGTTDEEDDDVEQEGAD 723
 |||||
 64 ESTSGPEDTRAASSNLNSGETESVKTMIVHDDVESEPA MTPSKEGTLIV 113
 |||||
 724 ESTSGPEDTRAASSNLNSGETESVKTMIVHDDVESEPA MTPSKEGTLIV 773
 |||||
 114 RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR 163
 |||||
 774 RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR 823
 |||||
 164 PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV 213
 |||||
 824 PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV 873
 |||||
 214 NLLVGTESGLMLLDRSGQGVYPLINRRRRFQQMDVLEGLNVLV TISGKKD 263
 |||||
 874 NLLVGTESGLMLLDRSGQGVYPLINRRRRFQQMDVLEGLNVLV TISGKKD 923
 |||||
 264 KLRVYLSWLNRKILHNDPEVEKKQGWTTVGDLEGCVHYKVVKYERIKFL 313
 |||||
 924 KLRVYLSWLNRKILHNDPEVEKKQGWTTVGDLEGCVHYKVVKYERIKFL 973
 |||||

FIG. 43

314	VIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLDLTVEEGQRLKVI	363
974	VIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLDLTVEEGQRLKVI	1023
364	YGSCAGFHAVDVGSGVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY	413
1024	YGSCAGFHAVDVGSGVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY	1073
414	EDEGVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVE	463
1074	EDEGVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVE	1123
464	TGHLDGVMHKRAQRLKFLCERNDKVFFASVRSQVYFMTLGRTSLL	513
1124	TGHLDGVMHKRAQRLKFLCERNDKVFFASVRSQVYFMTLGRTSLL	1173
	514 SW 515	
	1174 SW 1175	

FIG. 43 (CONT.)¹

64	LTANETQASSTLQKHKSSSFTPFIDPRLLQISPSGGTTVTSVVGFS	CD	113
	::		
771	LIVRQTQASSTLQKHKSSSFTPFIDPRLLQISPSGGTTVTSVVGFS	CD	820
	.		
114	GMRPEAIRQDPTRKGSVVNVNPTNRPQSDTPEIRKYKKRFNSEILCAAL		163
821	GMRPEAIRQDPTRKGSVVNVNPTNRPQSDTPEIRKYKKRFNSEILCAAL		870
	.		
164	WGVNLLVGTESGLMLDRSGQKVYPLINRRRQQQMDVLEGLNVLTISG		213
871	WGVNLLVGTESGLMLDRSGQKVYPLINRRRQQQMDVLEGLNVLTISG		920
	.		
214	KKDKLRYYLSWLNRNKILHNDPEVKKQGWTTVGDLEGCVHYKVVKYERI		263
921	KKDKLRYYLSWLNRNKILHNDPEVKKQGWTTVGDLEGCVHYKVVKYERI		970
	.		
264	KFLVIALKSSVEVYAWAPKPYHKFMAFKSFGEVLVHKPLLVDLTVEEGQRL		313
971	KFLVIALKSSVEVYAWAPKPYHKFMAFKSFGEVLVHKPLLVDLTVEEGQRL		1020

FIG. 44

314	KVIYGSCAGFHAVDVGSDVYDIYLP	THIQCSIKPHAIILPNTDGMELL	363
1021	KVIYGSCAGFHAVDVGSDVYDIYLP	THIQCSIKPHAIILPNTDGMELL	1070
364	VCYEDEGVYVNTYGRITKDVVLQW	GEMPTSVAYIRSNQTMGWGEKAIEIR	413
1071	VCYEDEGVYVNTYGRITKDVVLQW	GEMPTSVAYIRSNQTMGWGEKAIEIR	1120
414	SVETGHLDGVMHKRAQRLKFLCERN	DKVFASVRGGSSQVYFMTLGR	463
1121	SVETGHLDGVMHKRAQRLKFLCERN	DKVFASVRGGSSQVYFMTLGR	1170
	464	SLLSW	468
	1171	SLLSW	1175

FIG. 44 (CONT.¹)

```

1 MDCQLSILLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50
  |||||
1 MDCQLSILLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50
  |||||
51 GWEEISGVDEHYTPIRTYQVCNVMDSQNNWLR TNWVPRNSAQKIYVELK 100
  |||||
51 GWEEISGVDEHYTPIRTYQVCNVMDSQNNWLR TNWVPRNSAQKIYVELK 100
  |||||
101 FTLRDCNSIPLVLGTCKETFNLIYMESDDDDHG VKFREHQFTKIDTIAADE 150
  |||||
101 FTLRDCNSIPLVLGTCKETFNLIYMESDDDDHG VKFREHQFTKIDTIAADE 150
  |||||
151 SFTQMDLGDRILKLNTEIREVGPVNKKGFYLAQDVGCACVALSVRVYFK 200
  |||||
151 SFTQMDLGDRILKLNTEIREVGPVNKKGFYLAQDVGCACVALSVRVYFK 200
  |||||
201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNSEEDP PRMYCSTEGEW 250
  |||||
201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNSEEDP PRMYCSTEGEW 250
  |||||

```

FIG. 45

```

251 LVPIGKCSNAGYEERGFMCQACRPGFYKALDGNMKCAKCPHSSTQEDG 300
|||||
251 LVPIGKCSNAGYEERGFMCQACRPGFYKALDGNMKCAKCPHSSTQEDG 300
|||||

301 SMNCRCENNYFRADKDPSPMACTRPSPSRNVISNINETSVILDWSWPLD 350
|||||
301 SMNCRCENNYFRADKDPSPMACTRPSPSRNVISNINETSVILDWSWPLD 350
|||||

351 TGGRKDVTFNII CKKCGWNI KQCEPCSPNVRF LPRQFGLTNTTVTVDLL 400
|||||
351 TGGRKDVTFNII CKKCGWNI KQCEPCSPNVRF LPRQFGLTNTTVTVDLL 400
|||||

401 AHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLTIKKDRTSR 450
|||||
401 AHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLTIKKDRTSR 450
|||||

451 NSISLSWQEP EHPNGIILDYEVKY EKQEQT SYTILRARGTNVTISSLK 500
|||||
451 NSISLSWQEP EHPNGIILDYEVKY EKQEQT SYTILRARGTNVTISSLK 500
|||||

```

FIG. 45 (CONT.¹)

501	PDIIYVFQIRARTAAGYGTNSRKFETSPDFSISGESSQVVMIAISAA	550
501	PDIIYVFQIRARTAAGYGTNSRKFETSPDFSISGESSQVVMIAISAA	550
551	VAIIILTUVIYVLIGRFCGYKSKHGADKRLHFGNGHLKLPGLRTYVDPH	600
551	VAIIILTUVIYVLIGRFCGYKSKHGADKRLHFGNGHLKLPGLRTYVDPH	600
	601 TYEDPTQAVHEFAKELDATNISIDKVVGA	629
	601 TYEDPTQAVHEFAKELDATNISIDKVVGA	629

FIG. 45 (CONT.²)

256 KKHFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVDDDDCLKNSETMPPP 305
 |||||
 338 KKHFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVDDDDCLKNSETMPPP 387
 |||||
 306 THTAFSGHHLPEVGFYTTSSCVLSDRSCLRVTAGPTSLDLDVNVQRTLDN 355
 |||||
 388 THTAFSGHHLPEVGFYTTSSCVLSDRSCLRVTAGPTSLDLDVNVQRTLDN 437
 |||||
 356 NLATEAYERRIKRLEQEKLELSRKLQESTQTVQALQYSTVDGPLTASKDL 405
 |||||
 438 NLATEAYERRIKRLEQEKLELSRKLQESTQTVQALQYSTVDGPLTASKDL 487
 |||||
 406 EIKNLKEEI 414
 |||||
 488 EIKNLKEEI 496

FIG. 46 (CONT.¹)

```

1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVYQPRRKRAKLIKYL 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVYQPRRKRAKLIKYL 50

51 MGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKLRIPNGEANVKKEIQ 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 MGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKLRIPNGEANVKKEIQ 100

101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVEYCVCGMQEMLDSVPEKRFVP 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVEYCVCGMQEMLDSVPEKRFVP 150

151 CQAHG 155
  | | | |
151 CQAHG 155

```

FIG. 47

```

1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRKRKAKLIGKYL 50
  |||
1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRKRKAKLIGKYL 50
  |||
51 MGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKLRRIPNGEANVKKEIQ 100
  |||
51 MGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKLRRIPNGEANVKKEIQ 100
  |||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRPV 150
  |||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRPV 150
  |||
151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIPGNLLLTGGTLKISDLGVAE 199
  |||
151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIPGNLLLTGGTLKISDLGVAE 199
  |||

```

FIG. 48

27 VKDFLSQLRSSNRRESIPESGGGTEMDGFRRTIENQHSRNDVMVSEWLN 76
 |||||:|||||
 301 VKDFLSQLKSSNRRESIPESGGGTEMDGFRRTIENQHSRNDVMVSEWLN 350
 . . .
 77 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTP 126
 |||||
 351 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTP 400
 . . .
 127 TSTFRNQMPSPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 176
 |||||
 401 TSTFRNQMPSPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 450
 . . .
 177 NIYNCSGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPFPVGSQEGP 226
 |||||
 451 NIYNCSGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPFPVGSQEGP 500
 .
 227 KDPEAWSRPQGWYNHSGK 244
 |||||
 501 KDPEAWSRPQGWYNHSGK 518

FIG. 49

```

30 EEQARELYRRLREKPRDQTEGDSQEMVRLLLQAIQSFEEKVRVIYQLS 79
   |||||
564 EEQARELYRRLREKPRDQTEGDSQEMVRLLLQAIQSFEEKVRVIYQLS 613
   |||||

80 KTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 129
   |||||
614 KTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 663
   |||||

130 KVRGVPVSGSPDSMNASRLSQPGQLMSQSPSTASNSLPEPAKKEELVAEAEH 179
   |||||
664 KVRGVPVSGSPDSMNASRLSQPGQLMSQSPSTASNSLPEPAKKEELVAEAEH 713
   |||||

180 NLCTLLENAIQDQTVREQDQSFALDWSWLQTEEEHSCLEQAS 222
   |||||
714 NLCTLLENAIQDQTVREQDQSFALDWSWLQTEEEHSCLEQAS 756

```

FIG. 50

1	MRLTLCCCTWREERMGEESL	PVCASCGRIYDQYLOALNADH	ADCF	50	
1	MRLTLCCCTWREERMGEESL	PVCASCGRIYDQYLOALNADH	ADCF	50	
51	RCCDCSASLSHQY	KGDLCKKDYARYGESHC	SEQITKGLVMVAG	100	
51	RCCDCSASLSHQY	KGDLCKKDYARYGESHC	SEQITKGLVMVAG	100	
101	ELKYHPECFICLTCGTF	IGDGTTLVEH	SKLYCGHCYYQTVTPVIEQI	150	
101	ELKYHPECFICLTCGTF	IGDGTTLVEH	SKLYCGHCYYQTVTPVIEQI	150	
151	LPDSPGSHLPHTVTL	VSIPASSHGKRLSVS	IDPPHGP	PGCGTEHSHTVR	200
151	LPDSPGSHLPHTVTL	VSIPASSHGKRLSVS	IDPPHGP	PGCGTEHSHTVR	200
201	VQVDPGCMSPDVKN	SLHVGDRILEINGT	PIRNVPLDEIDL	LIQETSRL	250
201	VQVDPGCMSPDVKN	SLHVGDRILEINGT	PIRNVPLDEIDL	LIQETSRL	250

FIG. 51

251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
|||||
301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKG GCF 350
|||||
301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKG GCF 350
351 GQAIKV 356
|||||
351 GQAIKV 356

FIG. 51 (CONT.¹)

```

1  MRLLCCTWREERMGEESLPCVASCGRYYDGYLQALNADWHADCF 50
   |||||
1  MRLLCCTWREERMGEESLPCVASCGRYYDGYLQALNADWHADCF 50

51  RCCDCSASLSHQYEEKDGLFCKDYWARYGESCHGCSEQITKGLVMVAG 100
   |||||
51  RCCDCSASLSHQYEEKDGLFCKDYWARYGESCHGCSEQITKGLVMVAG 100

101 ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
   |||||
101 ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150

151 LPDSPGSHLPHTVTVLSIPASSHGKRGLSVSDPPHPPGCGTEHSHTVR 200
   |||||
151 LPDSPGSHLPHTVTVLSIPASSHGKRGLSVSDPPHPPGCGTEHSHTVR 200

201 VQGVDPGCMSPDVKNSTHVGDRIEINGTPIRNVPLDEIDLLIQETSRL 250
   |||||
201 VQGVDPGCMSPDVKNSTHVGDRIEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 51

```

251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||
301 RSPGAGSLGSPASQKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGKGF 350
|||||
301 RSPGAGSLGSPASQKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGKGF 350
|||||
351 GQAIKV 356
|||||
351 GQAIKV 356

```

FIG. 51 (CONT.¹)

```

1  MRLTLCCCTWREERMGEESGSELPVCASCGQRIYDGQYLQALNADWHADCF 50
  |||
1  MRLTLCCCTWREERMGEESGSELPVCASCGQRIYDGQYLQALNADWHADCF 50
  |||
51  RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||
51  RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||
101  ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
  |||
101  ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
  |||
151  LPDSPGSHLPHTVTLVSIIPASSHGKRGLSVSIIDPPHPPGCGTEHSHTVR 200
  |||
151  LPDSPGSHLPHTVTLVSIIPASSHGKRGLSVSIIDPPHPPGCGTEHSHTVR 200
  |||
201  VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
  |||
201  VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
  |||

```

FIG. 52

1 MASDAVQSEPRWSLLEQLGLACADLAAPGVQQQLELERERLRREIRKEL 50
 1 MASDAVQSEPRWSLLEQLGLACADLAAPGVQQQLELERERLRREIRKEL 50
 51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRDLLHQQLQELHAHVVL 100
 51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRDLLHQQLQELHAHVVL 100
 101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQIAIELKVKGAEENMIQ 150
 101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQIAIELKVKGAEENMIQ 150
 151 TYSNGSTKDRKLLLTAAQMLQDSKTIDIIRMQLRRALQADQLENQAAPD 200
 151 TYSNGSTKDRKLLLTAAQMLQDSKTIDIIRMQLRRALQAGQLENQAAPD 200
 201 DTQGSDDLGAVELRIEELRHHERVEHAEGAENVLRLLSAAKAPDRKAV 250
 201 DTQGSDDLGAVELRIEELRHHERVEHAEGAENVLRLLSAAKAPDRKAV 250

FIG. 53

```

251  SEAQKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
    |||
251  SEAQKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
    |||
301  STRLAGPPATHYSTICKPAPLTGTLVVRVVGCRDLPETIPWNPTPSMG 350
    |||
301  STRLAGPPATHYSTICKPAPLTGTLVVRVVGCRDLPETIPWNPTPSMG 350
    |||
351  PGTPDSRPPFLSRPARGLYSRGSLSGRSSLKAEAEENTSEVSTVLKLDNT 400
    |||
351  PGTPDSRPPFLSRPARGLYSRGSLSGRSSLKAEAEENTSEVSTVLKLDNT 400
    |||
401  VVGQTSWKPCGPNWDQSFTELEERARELELAVFWRDQGLCALKFLKLE 450
    |||
401  VVGQTSWKPCGPNWDQSFTELEERARELELAVFWRDQGLCALKFLKLE 450
    |||
451  DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQKG 500
    |||
451  DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQKG 500
    |||

```

FIG. 53 (CONT.¹)

501	AQARQMNI	DVATWVRLLRRLLPNATGTGTFSPGASPGSEARTTGD	ISV	550	
501	AQARQMNI	DVATWVRLLRRLLPNATGTGTFSPGASPGSEARTTGD	ISV	550	
551	EKINLGTDS	SSPQKSRRDPSSPSLSPIQUESTAPELPSETQTETGP	A	600	
551	EKINLGTDS	SSPQKSRRDPSSPSLSPIQUESTAPELPSETQTETGP	A	600	
601	LCSPLRKSPL	TLEDFKFLAVLGRGHFGKVLLSEFRPSGELEFAIKALKKG	D	650	
601	LCSPLRKSPL	TLEDFKFLAVLGRGHFGKVLLSEFRPSGELEFAIKALKKG	D	650	
651	IVARDEVESIM	CEKRILAAVT	SAGHPFLVNLFGCFQTPEHVCFVMEYSAG	700	
651	IVARDEVESIM	CEKRILAAVT	SAGHPFLVNLFGCFQTPEHVCFVMEYSAG	700	
701	GDLMLHIHSD	VFSEPRALFYSA	C.....	723	
701	GDLMLHIHSD	VFSEPRALFYSA	CVLGQLFHEHKIVYRDCLKLDNLLD	T	750

FIG. 53 (CONT.)²


```

723 ..... 723
751 EGYVKIADFLGCKEGMGYGDRTSTFCGTPEFLAPEVLTDTSYTRAVDWMG 800
723 ..... 723
801 LGVLLYEMLVGESPFPGDDEEEVFDIVNDEVYPRFLSAEAGIMRRL 850
724 .....RLPPFVPTLSGRD 738
      |||||
851 RRNPERRLGSSERDAEDVKKQPFRTLGWEALLARLPPPFVPTLSGRD 900
      .
739 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDDFVAGGC 780
      |||||
901 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDDFVAGGC 942

```

FIG. 53 (CONT.)

1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELEFERLRREIRKEL 50
 |||||
 1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELEFERLRREIRKEL 50
 |||||
 51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRDLHLHQQLQELHAHVVL 100
 |||||
 51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRDLHLHQQLQELHAHVVL 100
 |||||
 101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKGAEENMIQ 150
 |||||
 101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKGAEENMIQ 150
 |||||
 151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
 |||||
 151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQAGQLENQAAPD 200
 |||||
 201 DTQGSPDLGAVELRIEELRHHFRVEHAVAEGAKNVRLLSAAKAPDRKAV 250
 |||||
 201 DTQGSPDLGAVELRIEELRHHFRVEHAVAEGAKNVRLLSAAKAPDRKAV 250
 |||||

FIG. 54

```

251 SEAEKLTESNQKGLLREALERRIGELPADHPKGRLLREELAAASSAAF 300
|||||
251 SEAEKLTESNQKGLLREALERRIGELPADHPKGRLLREELAAASSAAF 300
|||||
301 STRIAGFPFATHYSTICKPAPLTGTLEVRVVGCRDLPETIPNPTPSMGG 350
|||||
301 STRIAGFPFATHYSTICKPAPLTGTLEVRVVGCRDLPETIPNPTPSMGG 350
|||||
351 PGTPDSRPFFLSRPARGLYRSGSLSGRSSLKAEAEENTSEVSTVLKLDNT 400
|||||
351 PGTPDSRPFFLSRPARGLYRSGSLSGRSSLKAEAEENTSEVSTVLKLDNT 400

```

FIG. 54 (CONT.¹)

FIG. 55

90 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRLLVKDP 139
 |||||
 211 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRLLVKDP 260
 |||||
 140 KRRMTIAQSLHSHWIKAIRRRNVRGEDSGRKPERRRLKTTTLKEYTIKSH 189
 |||||
 261 KRRMTIAQSLHSHWIKAIRRRNVRGEDSGRKPERRRLKTTTLKEYTIKSH 310
 |||||
 190 SSLPPNNSYADFERFSKVLEEEAAEEGIRELQSRRLCHEDVEALAAIY 239
 |||||
 311 SSLPPNNSYADFERFSKVLEEEAAEEGIRELQSRRLCHEDVEALAAIY 360
 |||||
 240 EEKEAWYREESDSLQDLRRLRQELLKTEALKRQAEAKGALLTSGLK 289
 |||||
 361 EEKEAWYREESDSLQDLRRLRQELLKTEALKRQAEAKGALLTSGLK 410
 |||||
 290 RRFSLRLENRYEALAKQVASEMRVQDLVRALEQEKLOGVECCGLR 333
 |||||
 411 RRFSLRLENRYEALAKQVASEMRVQDLVRALEQEKLOGVECCGLR 454

FIG. 56

```

61  GETALHKAACQNRNAVQCQLLVDAGASLRKTDGKGTPOERAQQAGDPDLA 110
    |||||
995 GETALHKAACQNRNAVQCQLLVDAGASLRKTDGKGTPOERAQQAGDPDLA 1044
    |||||
    111 AYLESRQNYKVIGHEDLETAV 131
    |||||
    1045 AYLESRQNYKVIGHEDLETAV 1065

```

FIG. 57

```

1 MRGAARLGRPRGRCI PCPAIRAPRPPRLJLLIALPLLPAGAAAAAPR 50
| | | | | | | | | | | | | | : | | | | |
1 MRGAARLGRPRGRCI PCPAIRAAAAP..ALLARCAVAAAGLRAAARPR 48

51 PPELQASAGPSVSLYLSEDEVRRLLIGLD AELYYVRNDLISHYALSFLL 100
| | | | | | | | | | | | | | | | | | | | | | | | | | |
49 PPELQASAGPSVSLYLSEDEVRRLLIGLD AELYYVRNDLISHYALSFNLL 98

101 VPSETNFLHTTHAKSVEYKLG FQVDNV LAMDMPQVNISVG EVPRTL S 150
| | | | | | | | | | | | | | | | | | | | | | | | | | |
99 VPSETNFLHTTHAKSVEYKLG FQVDNV LAMDMPQVNISVG EVPRTL S 148

151 VRFVELSCTGKV DSEVMILMQ LNLT VNSSKNFTVL NFKRRKM CYKKLEEV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | |
149 VRFVELSCTGKV DSEVMILMQ LNLT VNSSKNFTVL NFKRRKM CYKKLEEV 198

201 KTSALDKNTSR TIYPVHAAPT TSTRVF YISGVCCAVIFLVA I L AVLH 250
| | | | | | | | | | | | | | | | | | | | | | | | | | |
199 KTSALDKNTSR TIYPVHAAPT TSTRVF YISGVCCAVIFLVA I L AVLH 248

251 LHSMKRIELD D 261
| : | | | | | | | |

249 LHNMKRIELD D 259
```

FIG. 58

```

1  MPQVNISVQGEVPRTLVSVRVELSCTGKVDSEVMILQNLNTVNSSKNFT 50
   |||||
132 MPQVNISVQGEVPRTLVSVRVELSCTGKVDSEVMILQNLNTVNSSKNFT 181
   |||||
51  VLNFKRRKMCYKKEEVKTSALDKNTSRTIYDPVHAAPTSTRVFIYSVG 100
   |||||
182 VLNFKRRKMCYKKEEVKTSALDKNTSRTIYDPVHAAPTSTRVFIYSVG 231
   |||||
101 VCCAVIFLVAII LAVLHLHSMKRIELDDSI SASSSQGLSQPSTQTTQYL 150
   |||||
232 VCCAVIFLVAII LAVLHLHNMKRIELDDSI SASSSQGLSQPSTQTTQYL 281
   |||||
151 RADTPNNATPITSSYYPTLRIEKNDLRSVTLLEAKGVKDIAISRERITL 200
   |||||
282 RADTPNNATPITS..YPTLRIEKNDLRSVTLLEAKGVKDIAISRERITL 329
   |||||
201 KDVLEQGTGGRIFHGILIDEKDPNKEKQAFVKTVDQDASEIQVTMMILTES 250
   |||||
330 KDVLEQGTGGRIFHGILIDEKDPNKEKQAFVKTVDQDASEIQVTMMILTES 379

```

FIG. 59

251 CKLRGLHHRNLLPITHVCIEEGEKPVMILPYMNWGNLKLFLRQCKLVEAN 300
|||||
380 CKLRGLHHRNLLPITHVCIEEGEKPVMILPYMNWGNLKLFLRQCKLVEAN 429
|||||
301 NPQAISQQDLVHMAIQIACGMSYLAARREVIHKDLAARNCV 340
|||||
430 NPQAISQQDLVHMAIQIACGMSYLAARREVIHKDLAARNCV 469
|||||

FIG. 59 (CONT.¹)

FIG. 60

```

1  MELLQAEGATAVTGVPSPRATDPPSHL.....DGPPAVAVGQ 37
   |||||
519 MELLQAEGATAVTGVPSPRATDPPSHMARPWLWASARWWGQAPCTAATC 568
      |::|:
      |||

38  CPLVGP.GPMHRRHLLPARVP...RPGLSEALSILLFAVLSRAAALGC 83
   | | | | : || | | | | | | | | | | | | | | | | | |
569 CSLPGSLGLAYRR.....RFPCCSP.....LFCLVPPPPWAAALGW 603
      | | | | | | | | | | | | | | | | | | | | | | | |
      |::| |::| |::| |::| |::| |::| |::| |::| |::|
      84 IGLVAHAGQLTAVWRRRPGAARAP 106
      604 WPTPANSPQ.....SGAAQEP 619

```

FIG. 61

6 HEDFEFISGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYSLEKA 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
580 HEDEFEILGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYSLEKA 624

FIG. 62

[illegible]

FIG. 63

```

1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLLKTDGSGFIGYKEKPQVDLPYP 50
  |||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLLKTDGSGFIGYKEKPQVDLPYP 50
  |||||

51 LNNFSVASSVMFR 63
  |||||: :::
51 LNNFSVAKCQLMK 63

```

FIG. 64

[illegible]

FIG. 65

100

2


```

1 MELLRITYQPAASTKMCQALGKGCGNSKKRPPQPPEESQPPQSQAQ 50
   | | | | | | | | | | | | | | : | | | | | | | | | | | | | |
1 MELLRITYQPAASTKMCQALGKGCGGDSKKRPPQPPEESQPPQSQAQ 50

51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGVLGKGGFAKCYEFT 100
   | | | | | | | | | | | | | | : | | | | | | | | | | | | | |
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGVLGKGGFAKCYEFT 100

      101 DLTNKNKYAAKIIPHRSRVAKPHQREKVCMTLE 132
         | | | | | | | | | | | | | | : |
      101 DLTNKNKYAAKIIPHRSRVAKPHQREKIDKEIE 132
```

FIG. 67

```

1 MELLRTITYQPAASTKMCEQALGCGGNSKKRPPQPPEESQPPQSQAQ 50
  |||||
1 MELLRTITYQPAASTKMCEQALGCGGDSKKRPPQPPEESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHRSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHRSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYCSRR..VSVNSYLRTFAYPELTWYSKSLSGI 191
  |||||
151 DKENIYILLEYCSRRSMAHILKARKVLTEPEVRYLRQIVSGL 193

```

FIG. 68

```

1  MELLRTITYQPAASTKMCEQALGKCGGNSKKKRPPQPPEESQPPQSQAQ 50
  |||||
1  MELLRTITYQPAASTKMCEQALGKCGGDSKKKRPPQPPEESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
51 VPPAAPHHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHRSVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHRSVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYCSRR 165
  |||||
151 DKENIYILLEYCSRR 165

```

FIG. 69

[illegible]

FIG. 71

201 TYGLSAYSGKVRYICSAALGCRQWDSDEMEQEEDILLQRTQKTVRAGPR 250
 |||||
 201 TYGLSAYSGKVRYICSAALGCRQWDSDEMEQEEDILLQRTQKTVRAGPR 250
 |||||
 251 SGNEKNFVSGHFELRYIPDMETRAGFIESTFKPNENTEESKIISDVVEEQ 300
 |||||
 251 SGNEKNFVSGHFELRYIPDMETRAGFIESTFKPNENTEESKIISDVVEEQ 300
 |||||
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGKVI 350
 |||||
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGKVI 350
 |||||
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400
 |||||
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400
 |||||
 401 RISEKFPSPKALESVTNENAIIPLTIKWKPLIHSPRTPLVGSDEFD 450
 |||||
 401 RISEKFPSPKALESVTNENAIIPLTIKWKPLIHSPRTPLVGSDEFD 450

FIG. 71 (CONT.¹)

```

451 KCLSNDFKSHEEYSNGALSILQPYDNGYLYPYKRENRKSTQITVRF 500
|||||
451 KCLSNDFKSHEEYSNGALSILQPYDNGYLYPYKRENRKSTQITVRF 500
|||||
501 DNPHYNKNIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
|||||
501 DNPHYNKNIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
|||||
551 RKESETQCQTENKYDSVSGEANDSSWNNDIKNSGYISRYLTDFEPIQCLGR 600
|||||
551 RKESETQCQTENKYDSVSGEANDSSWNNDIKNSGYISRYLTDFEPIQCLGR 600
|||||
601 GGFGVVFEAKNKVDDCNAYAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650
|||||
601 GGFGVVFEAKNKVDDCNAYAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650
|||||
651 VRYFNWLEAPPEKWQEKMDIWLKDESTDWPLSSPSPMDAPSVKIRMD 700
|||||
651 VRYFNWLEAPPEKWQEKMDIWLKDESTDWPLSSPSPMDAPSVKIRMD 700
|||||

```

FIG. 71 (CONT.)²

```

701 PFSTKEHIEIIAPSPQSRSFVSGISCDQTSSSESQFSPLEFSGMDHEDI 750
|||||
701 PFSTKEHIEIIAPSPQSRSFVSGISCDQTSSSESQFSPLEFSGMDHEDI 750
|||||
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
|||||
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
|||||
801 TSSSIVFEDSGCDNASSKEEPTNRLHIGNHCANKLT 837
|||||
801 TSSSIVFEDSGCDNASSKEEPTNRLHIGNHCANKLT 837

```

FIG. 71 (CONT.)³

FIG. 72

```

210 . . . . . 210
251 VVLTPMKMVTTELAPLGSLDLRLKQGHFLGLTSLRYAVQVAEGMGYLE 300
210 . . . . . 210
301 SKRFIHRDLAARNLLLATRDLVKIGDFGLMRALPQNDDHYVMQEHKVPF 350
210 . . . . . 210
351 AWCAPESLKTRTFSHASDTWMFGVTIWEMFTYQGEPPWGLNGSQILHKID 400
210 . . . . . 210
401 KEGERLPRPDCPQDIYNVMVQCWAHKPEDRPTFVALRDFLEAQPTDMR 450

```

FIG. 72 (CONT.¹)

```

210 ..... 210
451 ALODFEEDKLHIQMNDVITIEGRAENYWWRGQTRTLCVGFPRNVVT 500
      .           .           .           .           .           .
210 ..... 210
501 SVAGLSAQDISOPLQNSFIHTGHGSDSDPRHCWGFPDRIDELYLGNPMDPP 550
      .           .           .           .           .           .
211 ..... PPQPAFFTQKPTYDPVSDDQDPLSSDFKRLGLRKPGLPR 249
      .           .           .           .           .           .
      III :: ||||| ||||| ||||| ||||| ||||| ||||| |||||
551 DLLSVELSTRPPQHLLGGVKKPTYDPVSDDQDPLSSDFKRLGLRKPGLPR 600
      .           .           .           .           .           .
250 GIWLAKPSARVPGTKASRGSGAEVTLIDFGEPEVPVALRPCAPSLAQLAM 299
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|:| |
601 GIWLAKPSARVPGTKASRGSGAEVTLIDFGEPEVP...PYGPAALPGAA 647
      .           .           .           .           .           .
300 DACSL..DETPQSPTRALPRELHPTPVVDWDARPLPPPAYDDVAQDE 347
      || :|:| :| ||||| ||||| ||||| ||||| ||||| |||||
648 GHGRLLPAGRDPASEPHAGTARPLHPTPVVDWDARPLPPPAYDDVAQDE 697

```

FIG. 72 (CONT.²)

348 DDFEICSINSTLVGAGVPAGPSQGQTNYAFVPEQARPPPLEDNLFPPQ 397
 |||||
 747
 698 DDFEICSINSTLVGAGVPAGPSQGQTNYAFVPEQARPPPLEDNLFPPQ 747
 |||||
 398 GGGKPPSSAQTAEIFQALQQECMRQLQAPAGSAPSPGGDDKPQVPPR 447
 |||||
 796
 748 GGGKPPSSAQTAEIFQALQQECMRQLQAP.GSPAPSPGGDDKPQVPPR 796
 |||||
 448 VPIPRPTRPHVQLSPAPPGEEETSQWPGPASPVRVPPREPLSPQGSRT 497
 |||||
 846
 797 VPIPRPTRPHVQLSPAPPGEEETSQWPGPASPVRVPPREPLSPQGSRT 846
 |||||
 498 SPLVPPGSSPLPRLSSSPGKTMTTQSFASDPKYATPQVIQAPGPRAG 547
 ||||| :||
 895
 847 SPLVPPGSSPLPRLSSSPGKTMTTQSFASDPKYATPQVIQAPG 895
 |||||
 548 CILPIVRDGKKVSTHYLLPERPSYERYQRFLEAQSPPEEPTLPVPL 597
 |||||
 896 CILPIVRDGKKVSTHYLLPERPSYERYQRFLEAQSPPEEPTLPVPL 945

FIG. 72 (CONT.³)

FIG. 72 (CONT.⁴)

[illegible]

FIG. 73

FIG. 73 (CONT.¹)

1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLLDDIKD 50
 |||||
 1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLLDDIKD 50
 51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNILKKSNNKLEELHHKL 100
 |||||
 51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNILKKSNNKLEELHHKL 100
 101 QELNAHIVVSDPEDITDCPRTPTPNNDPRCSTSNRLKALQQLDIELK 150
 |||||
 101 QELNAHIVVSDPEDITDCPRTPTPNNDPRCSTSNRLKALQQLDIELK 150
 151 VKQGAENMIQMYSSGSKDRKLHGTAAQQLLQDSKTKIEVIRMQILQAVQT 200
 |||||
 151 VKQGAENMIQMYSSGSKDRKLHGTAAQQLLQDSKTKIEVIRMQILQAVQT 200
 201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAGAKNMKLLGSGKVTD 250
 |||||
 201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAGAKNMKLLGSGKVTD 250

FIG. 74

251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300
 |||||G|||||
 251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300
 |||||G|||||
 301 ASPTLSPRQSMISTQNYSTLSKPAALTGTLEVRMLGCCQDILENVPGRSK 350
 |||||G|||||
 301 ASPTLSPRQSMISTQNYSTLSKPAALTGTLEVRMLGCCQDILENVPGRSK 350
 |||||G|||||
 351 ATSVLPWGPSPETRSSFMSRTSKSGSRNLLKTDDLSDNVCAVLKLD 400
 |||||G|||||
 351 ATSVLPWGPSPETRSSFMSRTSKSGSRNLLKTDDLSDNVCAVLKLD 400
 |||||G|||||
 401 NTVVGQTSWKPI SNQSDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 |||||G|||||
 401 NTVVGQTSWKPI SNQSDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 |||||G|||||

FIG. 74 (CONT.)¹

FIG. 74 (CONT.²)

```

1 MVSSQKLEKPIEMGSSEPLIADGDRRRKKRRRGRATDSLPGKFEDMYKL 50
  |||||
1 MVSSQKLEKPIEMGSSEPLIADGDRRRKKRRRGRATDSLPGKFEDMYKL 50
  |||||

51 TSELLGEGAYAKVQGVSLQNGKEYAVKIIEKQAGHSRSRVFREVETLYQ 100
  |||||
51 TSELLGEGAYAKVQGVSLQNGKEYAVKIIEKQAGHSRSRVFREVETLYQ 100
  |||||

101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGT 131
  |||||
101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGG 131
  |||||

```

FIG. 75

[illegible]

```

63 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDPLGKFEDMYKL 112
   |||||
1  MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDPLGKFEDMYKL 50
   |||||

113 TSELLGAYAKVQGA VSLQNGKEYAVKV 141
   |||||
51 TSELLGAYAKVQGA VSLQNGKEYAVKI 79

```

FIG. 76

```

1  MSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL 50
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
194 LGSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL 243

   . . . . .
51  WSLGVVLYIMLSGYPPFVGHCADCGWDRGEVCRVCQNKLFESI QEGKYE 100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
244 WSLGVVLYIMLSGYPPFVGHCADCGWDRGEVCRVCQNKLFESI QEGKYE 293

   . . . . .
101 FPKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVGQAPEKGLP 150
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
294 FPKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVGQAPEKGLP 343

   . . . . .
151 TPQVLQRNSSTMWDLTLFAAEAIALNRQLSQHEENELAEPEPALADGLCSM 200
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
344 TPQVLQRNSSTMWDLTLFAAEAIALNRQLSQHEENELAEPEPALADGLCSM 393

   . . . . .
201 KLSPPCKSRLARRRALAQAGGEDRSPTAL 231
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
394 KLSPPCKSRLARRRALAQAGGEDRSPTAL 424

```

FIG. 77

```

1 MRKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEV 50
  |||
1 MRKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEV 50
  |||
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
  |||
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
  |||
101 MEYCLGSASDLLLEVHKKPLQVEIAATHGALHGLAYLHSHALIHR 146
  |||
101 MEYCLGSASDLLLEVHKKPLQVEIAATHGALHGLAYLHSHALIHR 146
  |||

```

FIG. 78

```

2 MEELSLDPRRQELLEARFTGVGSKGPLNSESNNQSLCSVGLSDKEVE 51
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MEELSLDPRRQELLEARFTGVGSKGPLNSESNNQSLCSVGLSDKEVE 50

```

FIG. 79

27 KDLVEEEAEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 76
 |||||
 435 KDLVEEEAEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 484
 |||||
 77 CHLSAWAWASWPAAACTAGPKGRPPMTQVYERLEKLQAVVAGVPGHLEA 126
 | : : : : |||||
 485 CPPELGLGLQLACCCLHRRKRPPMTQVYERLEKLQAVVAGVPGHLEA 534
 |||||
 127 ASCI.PFPQENSIVSSTGRAHSGAAPWQPLAAPSGASAQAAEQLRGPNQ 175
 |||||
 535 ASCIPSPQENSIVSSTGRAHSGAAPWQPLAAPSGASAQAAEQLRGPNQ 584
 |||||
 176 PVESDESLGLSAAALRSWHLTPSCFLDPAPLREAGCPQGDTAGESSWGSG 225
 |||||
 585 PVESDESLGLSAAALRSWHLTPSCFLDPAPLREAGCPQGDTAGESSWGSG 634
 |||||
 226 PGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMVQKLALYEDGALDSL 275
 |||||
 635 PGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMVQKLALYEDGALDSL 684
 |||||
 276 QLLSSSSLPGLGLEQDRQGPKKVMNFRA 303
 |||||
 685 QLLSSSSLPGLGLEQDRQGPPEESDEFQS 712

FIG. 80

20 QTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL 69
 |||
 303 QTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL 352
 |||
 70 TPKLGDGFLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLA 119
 |||
 353 TPKLGDGFLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLA 402
 |||
 120 VDTDTFSGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEAGVALRST 169
 |||
 403 VDTDTFSGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEAGVALRST 452
 |||
 170 QSTLQAGLAADAWAAPIAMQIYKKHLDPGPGCHLSWAWAWASWPAAACT 219
 ||| : : :
 453 QSTLQAGLAADAWAAPIAMQIYKKHLDPGPGCPPELGLGLQACCLH 502
 |||
 220 AGPKGRPPMTQVYERLEKLAQVAVGVPGHLEAASCI.PFPQENSIVSSTG 268
 | |||
 503 RRAKRRPPMTQVYERLEKLAQVAVGVPGHLEAASCI.PFPQENSIVSSTG 552
 |||

FIG. 81

```

269 RAHSGAAPWQPLAAPSGASAAEQIQRGNQPVESDESLGGLSAALRSW 318
|||||
553 RAHSGAAPWQPLAAPSGASAAEQIQRGNQPVESDESLGGLSAALRSW 602
|||||
319 HLTSPCLDPAPLREAGCPQGDTAGESSWGSGPSRPTAVEGLALGSSAS 368
|||||
603 HLTSPCLDPAPLREAGCPQGDTAGESSWGSGPSRPTAVEGLALGSSAS 652
|||||
369 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQ 418
|||||
653 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQ 702

419 GPKKVMNFRA 428
||:: :|::
703 GPEESDEFQS 712

```

FIG. 81 (CONT.¹)

```

1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKMDALEPADWCQFAALIV 50
  ||||||||||||||||||||||||||||||||||||||||||||
1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKMDALEPADWCQFAALIV 50
  ||||||||||||||||||||||||||||||||||||||||||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADIVHILTHLQLLRARDIIT 100
  ||||||||||||||||||||||||||||||||||||||||||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADIVHILTHLQLLRARDIIT 100
  ||||||||||||||||||||||||||||||||||||||||||||
101 AWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSASTFLSPAFFGS 150
  ||||||||||||||||||||||||||||||||||||||||||||
101 AWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSASTFLSPAFFGS 150
  ||||||||||||||||||||||||||||||||||||||||||||
151 QTHSGPELGLVPSASLWPPPPSPAPSSSTKPGPESSVSLIQGARPSPFCW 200
  ||||||||||||||||||||||||||||||||||||||||||||
151 QTHSGPELGLVPSASLWPPPPSPAPSSSTKPGPESSVSLIQGARPSPFCW 200
  ||||||||||||||||||||||||||||||||||||||||||||

```

FIG. 82

```

201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMNTVYAVKRLKENADLEWT 250
|||||
201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMNTVYAVKRLKENADLEWT 250
|||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
|||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
|||||
301 HCQTQACPPLSWPQRLDILLGTARASQVSCNRVSSCVSKSSPGL 344
||||| : : : :
301 HCQTQACPPLSWPQRLDILLGTARAIQF.....LHQDSPSL 336

```

FIG. 82 (CONT.¹)

1 MFTEDVKFYLAELALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFG 50
 |||||
 164 MFTEDVKFYLAELALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFG 213
 |||||
 51 LSKESIDHEKKAYSFCGTVEYMAPEVNNRRGHTQSADWWSFGVLMFEMLT 100
 |||||
 214 LSKESIDHEKKAYSFCGTVEYMAPEVNNRRGHTQSADWWSFGVLMFEMLT 263
 |||||
 101 GTLPFQGGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMKRNPANRLGA 150
 |||||
 264 GTLPFQGGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMKRNPANRLGA 313
 |||||
 151 GPDGVEEIKRHSFESTIDWNKLYRREIHPFPKATGRPEDTFYFDPEFTA 200
 |||||
 314 GPDGVEEIKRHSFESTIDWNKLYRREIHPFPKATGRPEDTFYFDPEFTA 363
 |||||
 201 KTPKDSPIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHSIVQQLHR 250
 |||||
 364 KTPKDSPIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHSIVQQLHR 413
 |||||
 251 NSIQFTDGYEVKEDIGVGSYSVCKRCIHKATNMEFAVKV 289
 |||||
 414 NSIQFTDGYEVKEDIGVGSYSVCKRCIHKATNMEFAVKI 452
 |||||

FIG. 83

```

1 MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50
  |||
1 MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50
  |||
51 AITHHVKEGHEKADPSQFELLKVLGQSGFGKVFVLVKKISGSDARQLYAMK 100
  |||
51 AITHHVKEGHEKADPSQFELLKVLGQSGFGKVFVLVKKISGSDARQLYAMK 100
  |||
101 VLKATLKVDRDRVRTKMERDILVEVNHPPFIVKLHYAFQTEGKLYLILDFL 150
  |||
101 VLKATLKVDRDRVRTKMERDILVEVNHPPFIVKLHYAFQTEGKLYLILDFL 150
  |||
151 RGGDLFTRLKSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPE 197
  |||
151 RGGDLFTRLKSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPE 197
  |||

```

FIG. 84

FIG. 85

251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
 |||||
 251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
 |||||
 301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVETLEKLPFDLASHHH 350
 |||||
 301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVETLEKLPFDLASHHH 350
 |||||
 351 VKFHYAFALNRRNLPGDRAKALDIMPVQSEGQVADMYCLVGRIYKDM 400
 |||||
 351 VKFHYAFALNRRNLPGDRAKALDIMPVQSEGQVADMYCLVGRIYKDM 400
 |||||
 401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLAAGHQFESSF 450
 |||||
 401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLAAGHQFESSF 450
 |||||
 451 ELRKVG 456
 |||||
 451 ELRKVG 456

FIG. 85 (CONT.)


```

1 MREFVLKLNHNKIVKLF AIEEETTRHKVLIMEFCPCGSLYTVLEEPS 50
  |||||
53 MREFVLKLNHNKIVKLF AIEEETTRHKVLIMEFCPCGSLYTVLEEPS 102
  |||||

51 NAYGLPESEFLIVLRDVGGMNHIRENGIVHRDIKPGNIMRAL 93
  |||||
103 NAYGLPESEFLIVLRDVGGMNHIRENGIVHRDIKPGNIMRVI 145
  |||||

```

```

68 IGS.....AAYDAVLDRNVAIKLSRPFQNTAKRAYRELVMKCVN 110
   III      IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
70 IGSAGQIVCAAYDAVLDRNVAIKLSRPFQNTAKRAYRELVMKCVN 119
   III      IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
111 HKNIIISLNVFTPQKTLFEFQDVLVMEI LMDANLCQVIQWELDHERMSYL 160
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
120 HKNIIISLNVFTPQKTLFEFQDVLVMEI LMDANLCQVIQWELDHERMSYL 169
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
161 LYQMLCGIKHLHSAGIIHRDLKPSNIWVKS DCTILKILDFGLARTAGTSFM 210
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
170 LYQMLCGIKHLHSAGIIHRDLKPSNIWVKS DCTILKILDFGLARTAGTSFM 219
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
211 MTPYVVVTRYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYI 260
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
220 MTPYVVVTRYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYI 269
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
261 DQWNKVIEQLGTPCPEFMKKILOPTVRNYVENRPKYAGLTFPKLFPDSLFP 310
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
270 DOWNKVIEQLGTPCPEFMKKILOPTVRNYVENRPKYAGLTFPKLFPDSLFP 319
   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

```

FIG. 87

311 ADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINWVYDPAEVE 360
 |||||
 320 ADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINWVYDPAEVE 369
 |||||
 361 APPQIYDKQLDEREHTTEEWKELIYKEVMNSEKTKNGVVKGPSPSAQ 410
 |||||
 370 APPQIYDKQLDEREHTTEEWKELIYKEVMNSEKTKNGVVKGPSPSAQ 419
 |||||
 411 VQ 413
 |||||
 420 VQ 422

FIG. 87 (CONT.¹)

FIG. 88

FIG. 89

```

251 HSLPSDETFQNMNSKRKAETWKRNRQLAFSTVGTDPYIAPEVFMQTGYN 300
|||||
251 HSLPSDETFQNMNSKRKAETWKRNRQLAFSTVGTDPYIAPEVFMQTGYN 300
|||||
301 KLCDWWSLGVIMYEMMLIG 318
|||||
301 KLCDWWSLGVIMYEMMLIG 318

```

FIG. 89 (CONT.¹)

```

11 VSGGMLDIKIYIVNRGEHKNGLVEEAI IATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDIKIYIVNRGEHKNGLVEEAI IATILKEVLEGLDYLHRNGQIH 192
|||||
61 RDLKAGNILLGEDGSGVQIADFGVSAFLATGGDVTRNKVRKTFVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSGVQIADFGVSAFLATGGDVTRNKVRKTFVGTPCWMA 242
|||||
111 PEVMEQVRGYDFKADMWISFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWISFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 292
|||||
161 PTLETGVEDKEMMKYKSFRLKLSLCLQKDPKSRPTAAELLKCKFFQKA 210
|||||
293 PTLETGVEDKEMMKYKSFRLKLSLCLQKDPKSRPTAAELLKCKFFQKA 342
|||||
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEGDGWESDDDEM 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEGDGWESDDDEM 392

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FIG. 90

261 EKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQISLSVHDSQGPPNA 310
 |||||
 393 EKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQISLSVHDSQGPPNA 442
 |||||
 311 NEDYREASSCAVNLVLRNRSRKEINDIRFEFTPGRDTADGVSQELFSAG 360
 |||||
 443 NEDYREASSCAVNLVLRNRSRKEINDIRFEFTPGRDTADGVSQELFSAG 492
 |||||
 361 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCGSEIPDEVKLIGFA 410
 |||||
 493 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCGSEIPDEVKLIGFA 542
 |||||
 411 QLSVS 415
 |||||
 543 QLSVS 547

FIG. 90 (CONT.¹)


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11 VSGGMLDIKIYIVNRGEHKNVLEAEIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDIKIYIVNRGEHKNVLEAEIATILKEVLEGLDYLHRNGQIH 192
.
61 RDLKAGNILLGEDGSGVQIADFGVSAFLATGGDVTRNKVRKTFVGTFCWMA 110
|||||
193 RDLKAGNILLGEDGSGVQIADFGVSAFLATGGDVTRNKVRKTFVGTFCWMA 242
.
111 PEVMEQVRGYDFKADMWSFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 292
.
161 PTLTGVEDKEMMKYKGSFRKLLSLCLQDPSKRPTAAELLKCKFFQKA 210
|||||
293 PTLTGVEDKEMMKYKGSFRKLLSLCLQDPSKRPTAAELLKCKFFQKA 342
.
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 392

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FIG. 91

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. . .  
261 EKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQSLSVHDSQGPPNA 310  
. . .  
393 EKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQSLSVHDSQGPPNA 442  
  
311 NEDYREASSCAVNVLRLNRSRKELNDIRFEFTPGRDTADGVSQELFSAG 360  
. . .  
443 NEDYREASSCAVNVLRLNRSRKELNDIRFEFTPGRDTADGVSQELFSAG 492
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361 LVDGHDWVIVAANLQKIVDDPKALKTLTFKL 391
493 LVDGHDWVIVAANLQKIVDDPKALKTLTFKL 523

FIG. 91 (CONT.¹)